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U.S. Appln. No. 10/618,963

IN THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

Claims 1-25. (Cancelled)

Claim 26. (Currently amended) A method of sequencing all or part of a target nucleic acid molecule comprising the steps of:

- (A) determining the sequence of a portion of said target nucleic acid molecule by identifying magnifying tags associated with said portion of the target nucleic acid molecule, wherein said magnifying tags represent a detectable signal or sequence that corresponds to one or more bases of said portion;
- (B) determining the position of said portion within said target nucleic acid molecule; and
- (C) combining the information obtained in steps (A) and (B) to obtain the sequence of all or part of said target nucleic acid molecule.

Claim 27. (Previously Presented) The method as claimed in Claim 26, wherein said position is determined by reference to a positional marker.

Claim 28. (Previously Presented) The method as claimed in Claim 26, wherein said position is determined by reference to a restriction map of said target nucleic acid molecule.

Claim 29. (Previously Presented) The method as claimed in Claim 26, wherein the portion which is sequenced has 4 or more nucleotide bases and/or the position of said portion within said

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target nucleic acid molecule is determined with an accuracy of less than 1 kb.

Claim 30. (Previously Presented) The method as claimed in Claim 26, wherein said portion is sequenced by identifying magnifying tags associated with the target nucleic acid molecule, wherein said magnifying tags correspond to one or more bases of an adapter binding region or to one or more bases in proximity to an adapter binding region, wherein said adapter binding region binds an adapter molecule which comprises:

- (i) one or more of said magnifying tags, or
- (ii) a means for attaching one or more of said magnifying tags.

Claim 31. (Previously Presented) The method as claimed in Claim 26, wherein the sequence of the target nucleic acid molecule is determined by assessing the complementarity of a portion of said target nucleic acid molecule by a process comprising the steps of:

- (i) treating said target nucleic acid molecule so that at least a region of said target nucleic acid molecule is converted into a form suitable for binding a complementary probe, wherein said complementary probe is bound to a solid support or said complementary probe carries a means for attaching to a solid support;
- (ii) binding said complementary probe to at least a portion of said region suitable for binding a complementary probe;
- (iii) optionally repeating steps (i) and (ii), with the proviso that said complementary probe binds to an

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adjacent or overlapping region of said target nucleic acid molecule relative to the region to which the complementary probe of the previous cycle bound; and

- (iv) determining the sequence of said target nucleic acid molecule by identifying the complementary probe(s) to which said target nucleic acid molecule bound.

Claim 32. (Previously Presented) The method as claimed in Claim 31, wherein in step (i) said form is a single-stranded nucleic acid molecule.

Claim 33. (Previously Presented) The method as claimed in Claim 31, wherein in step (ii) said portion is 4 to 12 nucleotide bases in length.

Claim 34. (Previously Presented) The method of as claimed in Claim 26, wherein a portion of said sequence is determined by identifying magnifying tags associated with the target nucleic acid molecule, wherein said magnifying tags correspond to one or more bases of an adapter binding region or to one or more bases in proximity to an adapter binding region, wherein said adapter binding region binds an adapter molecule which comprises:

- (i) one or more of said magnifying tags, or
- (ii) a means for attaching one or more of said magnifying tags; and

an adjacent or overlapping portion of said sequence is determined by a process comprising the steps of:

- (i) treating said target nucleic acid molecule so that a region of said target nucleic acid molecule is converted into a form suitable for

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- binding a complementary probe, wherein said complementary probe is bound to a solid support or said complementary probe carries a means for attaching to a solid support;
- (ii) binding said complementary probe to at least a portion of said region suitable for binding a complementary probe;
 - (iii) optionally repeating steps (i) and (ii), with the proviso that said complementary probe binds to an adjacent or overlapping region of said target nucleic acid molecule relative to the region to which the complementary probe of the previous cycle bound; and
 - (iv) determining the sequence of said target nucleic acid molecule by identifying the complementary probe(s) to which said target nucleic acid molecule bound.

Claim 35. (Previously Presented) The method as claimed in Claim 26, wherein said method is performed on a sample comprising a heterogeneous mixture of target nucleic acid molecules.

Claim 36. (Previously Presented) A method of producing a map of a target nucleic acid molecule comprising the steps of:

- (A) obtaining sequence information on portions of a target nucleic acid molecule by cleaving said target nucleic acid molecule with one or more nucleases; and
- (B) binding an adapter molecule to a region of said target nucleic acid molecule, wherein said

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adapter molecule comprises one or more magnifying tags as claimed in claim 26,
wherein each tag comprises:

- (i) a first signaling moiety which corresponds to one or more bases of said region to which said adapter molecule binds, and
- (ii) a second signaling moiety which corresponds to a nuclease used for cleavage,

wherein said portions comprise all or part of the cleavage sites of said nucleases and/or all or part of the restriction sites of said nucleases;
and

- (C) determining the position of said portions within said target nucleic acid molecule so to produce a map of the target nucleic acid molecule.

Claim 37. (Previously Presented) The method as claimed in Claim 36, wherein said nuclease has a cleavage site which is separate from its recognition site.

Claim 38. (Previously Presented) The method as claimed in Claim 36, wherein said cleaving produces complementary single-stranded regions.